

SCORE Search Results Details for Application 10804772 and Search Result us-10-804-772- 1.rng.

[Score Home
Page](#)

[Retrieve Application
List](#)

[SCORE System
Overview](#)

[SCORE
FAQ](#)

[Comments /
Suggestions](#)

This page gives you Search Results detail for the Application 10804772 and Search Result us-10-804-772-1.rng.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2006, 11:41:24 ; Search time 2548 Seconds
(without alignments)
18848.056 Million cell updates/sec

Title: US-10-804-772-1

Perfect score: 6888

Sequence: 1 atgtgggtattatattgtt.....cctagttcaggccaaagctt 6888

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
	1	6888	100.0	6888	3	AAA59599
	2	3379	.49.1	3379	14	AED95597
	3	669	9.7	1035	14	AED95588
c	4	140.4	2.0	8056	8	ABZ10246
	5	136.4	2.0	8056	8	ABZ10246
	6	135.6	2.0	6508	10	ADF31314
	7	132.8	1.9	1509	14	AED95599
	8	132.8	1.9	1521	12	ADK14855
	9	127.8	1.9	2066	13	ADX64858
c	10	124	1.8	8056	8	ABZ10100
	11	123.2	1.8	8056	8	ABZ10100
c	12	112.2	1.6	2482	14	ADZ71091
	13	107	1.6	2131	14	ADZ71009
c	14	107	1.6	2131	14	ADZ71009
	15	102.6	1.5	2482	14	ADZ71091
	16	94.6	1.4	1181	9	Ach03759
	17	94.2	1.4	1428	14	ADZ70899
	18	94.2	1.4	1554	14	ADZ70999
	19	93.8	1.4	1524	14	ADZ70897
	20	93.8	1.4	4660	14	ADZ70902
	21	92.8	1.3	4937	2	AAT85307
c	22	91.6	1.3	960	11	ACN85231
	23	91.2	1.3	828	14	ADZ70929
	24	91.2	1.3	1367	14	ADZ70967
c	25	91.2	1.3	1428	14	ADZ70899
	26	89.8	1.3	115218	8	Aca64845
c	27	89.6	1.3	1554	14	ADZ70999
c	28	89.6	1.3	110000	13	ABD32968_6
c	29	89.2	1.3	4660	14	ADZ70902
c	30	88.8	1.3	1169	14	ADZ71002
	31	88.2	1.3	453	9	Ach03747
c	32	88.2	1.3	5286	13	ADS89278
c	33	88.2	1.3	5286	13	ADS89552
	34	87.6	1.3	568	10	ABX56964
	35	87.6	1.3	1419	6	ABZ12814
	36	87.6	1.3	1608	2	AAT85306
	37	87.6	1.3	1646	3	AAC48157
	38	87.6	1.3	1649	3	AAC47986
	39	87.6	1.3	1649	15	Aef30128
	40	87.6	1.3	1682	15	AEG09798
c	41	87.4	1.3	158001	12	ADL17884
c	42	86.4	1.3	38678	14	AEB32373
c	43	86.4	1.3	38684	14	AEB32391
	44	86.4	1.3	158001	12	ADL17884
	45	86.2	1.3	5286	13	ADS89552

ALIGNMENTS

RESULT 1
AAA59599